(FILE 'HOME' ENTERED AT 11:09:22 ON 27 OCT 2004)

FILE 'MEDLINE, CAPLUS, BIOSIS, AGRICOLA' ENTERED AT 11:09:29 ON 27 OCT 2004

L1	7	S	CUVULARIA
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L2 0 S L1 AND PALLESCENS

L3 861 S PALLESCENS

L4 0 S OXIDOREDUCTASE AND L3

L5 23 S L3 AND OXI?

L6 20 DUP REM L5 (3 DUPLICATES REMOVED)

=>

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	% Query Match	Length	DB	ID	Description
-				-		
1	3336	100.0	627	4	US-09-468-578-7	Sequence 7, Appli
2	3336	100.0	627	4	US-09-868-839-7 6,509,309	Sequence 7, Appli
3	3168	95.0	627	4	US-09-468-578-4	Sequence 4, Appli
4	3168	95.0	627	4	US-09-868-839-4	Sequence 4, Appli
5	1929.5	57.8	594	4	US-09-468-578-2	Sequence 2, Appli
6	1929.5	57.8	594	4	US-09-218-702-2	Sequence 2, Appli
7	1929.5	57.8	594	4	US-09-868-839-2	Sequence 2, Appli
8	1795	53.8	572	3	US-09-401-476-4	Sequence 4, Appli
9	1776	53.2	568	4	US-09-218-702-4	Sequence 4, Appli



Database :

A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*

7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		ક				
Result		Query				
No.	Score	Match	Length	DB	ID	Description
1	3336	100.0	627	3	AAY96763	Aay96763 Curvulari
2	3336	100.0	627	3	AAY95539	Aay95539 Curvulari
3	3336	100.0	627	5	AA018212	Aao18212 C pallesc
4	3168	95.0	627	3	AAY96762	Aay96762 Bipolaris
5	3168	95.0	627	3	AAY95538	Aay95538 Bipolariu
6	3168	95.0	627	5	AA018211	Aao18211 B spicife
7	3168	95.0	627	6	ABG75578	Abg75578 B. spicif
8	2548	76.4	480	6	ABG75579	Abg75579 C. palles
9	1929.5	57.8	594	2	AAY45222	Aay45222 Stachybot
10	1929.5	57.8	594	2	AAY39992	Aay39992 Stachybot
11	1929.5	57.8	594	3	AAY96761	Aay96761 Stachybot
12	1929.5	57.8	594	3	AAY95537	Aay95537 Stachybot
13	1929.5	57.8	594	5	AAO18210	Aao18210 S chartar
14	1929.5	57.8	594	6	ABG75577	Abg75577 S. charta
15	1795	53.8	572	2	AAR40843	Aar40843 Bilirubin
16	1761.5	52.8	602	3	AAY69204	Aay69204 Amino aci
17	1743.5	52.3	583	5	AAU97316	Aau97316 Phenol ox
18	1743.5	52.3	583	5	ABB75770	Abb75770 Phenol ox

```
RESULT 2
AAY95539
    AAY95539 standard; protein; 627 AA.
ID
XX
AC
     AAY95539;
XX
DT
     10-OCT-2000 (first entry)
XX
     Curvularia pallescens phenol oxidising enzyme.
DE
XX
KW
     Phenol oxidising enzyme; detergent; bleaching.
XX
     Curvularia pallescens.
OS
XX
     WO200039306-A2.
PN
XX
PD
     06-JUL-2000.
XX
PF
     20-DEC-1999;
                    99WO-EP010287.
XX
PR
     23-DEC-1998;
                    98US-00220871.
PR
     23-JUN-1999;
                    99US-00338723.
XX
PA
     (UNIL ) UNILEVER NV.
PΑ
     (UNIL ) UNILEVER PLC.
PΑ
     (HIND-) HINDUSTAN LEVER LTD.
XX
     Bodie EA, Van Der Velden S, De Vries CH, Wang H;
PΙ
XX
     WPI; 2000-514528/46.
DR
     N-PSDB; AAA50021.
DR
XX
     Detergent composition comprising novel phenol oxidizing enzyme obtained
PT
     from fungus or bacteria, useful for pulp and paper bleaching, bleaching
PT
     color of stains on fabric and for anti-dye redeposition.
PT
XX
     Claim 8; Fig 10; 45pp; English.
PS
XX
     The present sequence is that of the Curvularia pallescens phenol
CC
     oxidising enzyme. The invention relates to detergent compositions
CC
     comprising novel phenol oxidising enzymes that have at least 60% identity
CC
     with the phenol oxidising enzyme of Stachybotrys chartarum (see
CC
     AAY95537), and which are obtained from a bacterium, yeast or non-
CC
     Stachybotrys fungus, especially C. pallescens, Bipolarius spicifera (see
CC
     AAY95538) and Amerosporium atrum (see AAY95540). The phenol oxidising
CC
     enzyme is capable of modifying the colour associated with dyes or
CC
     coloured compounds, and can be used for pulp and paper bleaching, for
CC
     bleaching the colour of stains on fabric and for anti-dye transfer in
CC
     detergent and textile applications. It may also be capable of modifying
CC
     the colour in the absence or presence of an enhancer. Expression vectors
CC
     and host cells comprising a nucleic acid encoding a phenol oxidising
CC
     enzyme, methods for producing the phenol oxidising enzyme, and methods
CC
     for constructing expression hosts are provided
CC
XX
SQ
     Sequence 627 AA;
                          100.0%; Score 3336; DB 3; Length 627;
  Query Match
```

	Best Loc Matches		Simila 7; Co	_			0;		No. matcl		e-307; 0;	Inc	dels		0;	Gaps	0 ;
Qy Db				11111	1111	Ш			1111	$\square \square \square$		111				FRILKD FRILKD	
Qу	,	61	WQSPE	YPILF	'REALI	PIPPA	KEP	NKMT	NPVTI	NKEIW	YYYEIV	/IKPE	FNQQ' 	VYPS	SLRP.	ARLVGY	120
Db)	61	WQSPE	YPILF	'REALI	PIPPA	KEP	NKMT.	NPVTI	NKEIV	YYYEIV	İKPI	YQQN	VYPS	LRP.	ARLVGY	120
Qу	,		11111	11111	+111	\square		1111		11111						FKDYYY	
DŁ)	121	DGISF	GPTII	VPRG'	TEAV	/RFV	NQGD	RESS	IHLHC	SPSRA	PFDO	SWAE	DLI	ИKGQ	FKDYYY	180
QΣ	7			11111			\square		1111	11111		111				VLSSKF	240
Dk)	181	PNNQA	ARFLW	YHDH	AMHV	raen	IAYFG	QAGA	YLITI	PAEDA	LĠĹ	SGY	GKYI	OIPL	VLSSKF	240
QΣ	7	241	YNSDG	TLQTS	VGEDI	NSLW(JDVI	HVNG	QPWP:	FFNVE	EPRKYF	RLRFI	'AAN'	vsri 	NFAL	YFVKQQ 	300
Dh		241	YNSDG	TLQTS	VGED	ทรเพต	3DVI	HVNG	QPWP:	FFNVI	EPRKYF	LRF	LNAA'	VSRI	NFAL	YFVKQQ	300
QΣ	7	301	ATATE	LPFQV	/IASD	AGLL:	THPV	QTSD	IYVA.	AAERY	YEIVFI	FAP:	YAGQ'	TIDI	LRNF	akangv 	360
Dŀ)	301	ATATE	LPFQ	/IASD	AGLL'	THPV	OTSD	İŸVA	AAER	YEIVFI	FAP	YAGQ'	TID	LRNF	AKANGV	360
Q١	!	361	GTDDI	TANT	KVMR	FHVS:	SQAV 	VDNS	VVPA	QLSQI	IQFPAI	KTG:	IDHH	FRF1	HRTN	SEWRIN	420
Dì)	361	GTDDI	TVAYO	KVMR	FHVS	SQAV	VDNS	VVPA	QLSQ:	IQFPAI)KTG	IDHH	FRF	HRTN	SEWRIN	420
Q۲	<i>!</i>	421	GIGFA	ADVQNF	RILAK	VPRG'	TVEI	WELE	NSSG	GWSHI	PIHVHI	VDF	RVVA 	RYGI	DEST	RGVMPY	480
Dŀ)	421	GIGF	ADVQNE	RILAK	VPRG'	TVEI	WELE	NSSG	ĠWŚĦI	PIHVHI	LVDF	RVVA	RYG:	DEST	RGVMPY	480
Q	7	481	ESAGI	KDVV	VLGRH	ETVL'	VEAH	HYAPW	DGVY	MFHCI	HNLIHI	EDQDI	AAMM 	FDV'	TKLQ 	NFGYNE	540
Dŀ	o	481	ESAGI	LKDVVV	VLGRH	ETVL	VEAL	HYAPW	IDĠVŸ	MFHCI	HNLIH	EDQDI	MMAA	FDV	rkLQ	NFGYNE	540
Q	Y	541	TTDF	HDPEDS	SRWSA	RPFT	AADI	TARS	GIFS	EASII	RARVNI	ELAL	EQPY 	SEL.	TVQA 	ASLEQY	600
D)	0	541	TTDF	IDPEDS	SRWSA	RPFT	AADI	TARS	GIFS	EASI	RARVNI	ELAL	EQPY	SEL.	AQVT	ASLEQY	600
Q	Y	601	YKTNI	KKRQAI				YRRFÇ	0V 62 	7							
D]	0	601	YKTNI					YRRFC	V 62	7							

.

```
RESULT 3
AA018212
    AA018212 standard; protein; 627 AA.
ID
XX
AC
    AAO18212;
XX
DT
    13-SEP-2002 (first entry)
XX
DE
    C pallescens phenol oxidising enzyme.
XX
    Phenol oxidising enzyme; enzyme; fungus; redox reaction; detergent;
KW
    paper industry; pulp industry; textile; food industry.
KW
XX
OS
    Curvularia pallescens.
XX
PN
    US6399329-B1.
XX
PD
    04-JUN-2002.
XX
PF
    21-DEC-1999;
                  99US-00468578.
XX
PR
    12-DEC-1998;
                   98US-00220871.
PR
    23-JUN-1999;
                  99US-00338723.
XX
     (GEMV ) GENENCOR INT INC.
PΑ
XX
    Wang H, Bodie EA;
PI
XX
DR
    WPI; 2002-498835/53.
DR
    N-PSDB; AAL47585.
XX
    New polynucleotides encoding phenol oxidizing enzymes, useful for
PT
    preventing the transfer of dyes in solution from one textile to another
PT
PT
    during detergent washing.
XX
PS
    Example 5; Fig 10; 37pp; English.
XX
    The present invention provides the protein and coding sequences of phenol
CC
    oxidising enzymes from Stachybotrys chartarum, Bipolaris spicifera and
CC
CC
    Curvularia pallescens. These enzymes are useful in the textiles, paper,
    pulp, detergent and food industries. In particular they are useful for
CC
    preventing the transfer of dyes in solution from one textile to another
CC
    during detergent washing (dye transfer inhibition). The present sequence
CC
    is the C. pallescens phenol oxidising enzyme
CC
XX
SO
    Sequence 627 AA;
 Query Match
                        100.0%;
                                 Score 3336; DB 5; Length 627;
 Best Local Similarity 100.0%;
                                Pred. No. 5.5e-307;
                                                             0; Gaps
                                                                         0;
 Matches 627; Conservative
                               0; Mismatches
                                                0; Indels
           1 MVAKYLFSALQLASIAKGIYGVALSERPAKYIDETPDEEKAALAAIVEDDPADVFRILKD 60
QУ
             1 MVAKYLFSALQLASIAKGIYGVALSERPAKYIDETPDEEKAALAAIVEDDPADVFRILKD 60
Db
          61 WOSPEYPILFREALPIPPAKEPNKMTNPVTNKEIWYYEIVIKPFNQQVYPSLRPARLVGY 120
Qу
```

Db	61	WQSPEYPILFREALPIPPAKEPNKMTNPVTNKEIWYYEIVIKPFNQQVYPSLRPARLVGY	120
Qy	121	DGISPGPTIIVPRGTEAVVRFVNQGDRESSIHLHGSPSRAPFDGWAEDLIMKGQFKDYYY	180
Db	121	DGISPGPTIIVPRGTEAVVRFVNQGDRESSIHLHGSPSRAPFDGWAEDLIMKGQFKDYYY	180
Qy	181	PNNQAARFLWYHDHAMHVTAENAYFGQAGAYLITDPAEDALGLPSGYGKYDIPLVLSSKF	240
Db	181	PNNQAARFLWYHDHAMHVTAENAYFGQAGAYLITDPAEDALGLPSGYGKYDIPLVLSSKF	240
Qy	241	YNSDGTLQTSVGEDNSLWGDVIHVNGQPWPFFNVEPRKYRLRFLNAAVSRNFALYFVKQQ	300
Db	241	YNSDGTLQTSVGEDNSLWGDVIHVNGQPWPFFNVEPRKYRLRFLNAAVSRNFALYFVKQQ	300
Qy	301	ATATRLPFQVIASDAGLLTHPVQTSDIYVAAAERYEIVFDFAPYAGQTIDLRNFAKANGV	360
Db	301	ATATRLPFQVIASDAGLLTHPVQTSDIYVAAAERYEIVFDFAPYAGQTIDLRNFAKANGV	360
QУ	361	GTDDDYANTDKVMRFHVSSQAVVDNSVVPAQLSQIQFPADKTGIDHHFRFHRTNSEWRIN	420
Db	361	GTDDDYANTDKVMRFHVSSQAVVDNSVVPAQLSQIQFPADKTGIDHHFRFHRTNSEWRIN	420
QУ	421	GIGFADVQNRILAKVPRGTVELWELENSSGGWSHPIHVHLVDFRVVARYGDESTRGVMPY	480
Db	421	GIGFADVQNRILAKVPRGTVELWELENSSGGWSHPIHVHLVDFRVVARYGDESTRGVMPY	480
Qy	481	ESAGLKDVVWLGRHETVLVEAHYAPWDGVYMFHCHNLIHEDQDMMAAFDVTKLQNFGYNE	540
Db	481	ESAGLKDVVWLGRHETVLVEAHYAPWDGVYMFHCHNLIHEDQDMMAAFDVTKLQNFGYNE	540
Qy	541	TTDFHDPEDSRWSARPFTAADLTARSGIFSEASIRARVNELALEQPYSELAQVTASLEQY	600
Db	541	TTDFHDPEDSRWSARPFTAADLTARSGIFSEASIRARVNELALEQPYSELAQVTASLEQY	600
Qy	601	YKTNKKRQAECEDMPAGPIPRYRRFQV 627	
Db	601		

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```
RESULT 4
AAY96762
    AAY96762 standard; protein; 627 AA.
ID
XX
AC
    AAY96762;
XX
DT
    09-OCT-2000 (first entry)
XX
    Bipolaris spicifera phenol oxidizing enzyme.
DE
XX
    Phenol oxidizing enzyme; colour; dye; modification; detergent; stain;
KW
    pulp; paper bleaching.
KW
XX
    Bipolaris spicifera.
OS
XX
    WO200037654-A2.
PN
ХX
PD
    29-JUN-2000.
XX
PF
     20-DEC-1999;
                   99WO-US031009.
XX
PR
     23-DEC-1998;
                   98US-00220871.
PR
     23-JUN-1999;
                   99US-00338723.
XX
PA
     (GEMV ) GENENCOR INT INC.
XX
ΡI
     Wang H, Bodie EA;
XX
     WPI; 2000-452191/39.
DR
     N-PSDB; AAA51315.
DR
XX
     New phenol oxidizing enzyme for modifying colors associated with dyes or
PT
     colored compounds, is obtained from fungus and is encoded by a nucleic
PT
     acid comprising a specific nucleotide sequence.
PT
XX
     Claim 8; Fig 3; 45pp; English.
PS
XX
     This sequence is the Bipolaris spicifera phenol oxidizing enzyme. Phenol
CC
     oxidizing enzymes encoded by nucleic acid sequences which hybridize to
CC
     the Stachybotrys chartarum DNA (AAA51313) are claimed, as long as the
CC
     enzyme is capable of modifying the colour associated with dyes or
CC
     coloured compounds. The enzymes are useful in detergent compositions and
CC
     for modifying colors associated with dyes or coloured compounds which
CC
     occur in stains in a sample. The enzymes are also useful for pulp and
CC
     paper bleaching, anti-dye transfer in detergent and other textile
CC
CC
     applications
XX
SO
     Sequence 627 AA;
                         95.0%; Score 3168; DB 3; Length 627;
  Query Match
                         92.8%; Pred. No. 4.9e-291;
  Best Local Similarity
                                                                           0;
                                                                0; Gaps
  Matches 582; Conservative 25; Mismatches
                                                 20; Indels
            1 MVAKYLFSALQLASIAKGIYGVALSERPAKYIDETPDEEKAALAAIVEDDPADVFRILKD 60
Qу
              1 MVAKYLFSALQLVSIAKGIYGVALSERPAKFVDNTPDEEKAALASIVEDDPADVVNMLKD 60
Db
```

QУ	61	WQSPEYPILFREALPIPPAKEPNKMTNPVTNKEIWYYEIVIKPFNQQVYPSLRPARLVGY	120
Db	61	WQSPEYPLIFRQPLPIPPAKEPNKLTNPVTNKEIWYYEIVIKPFTQQVYPSLRPARLVGY	120
Qy	121	DGISPGPTIIVPRGTEAVVRFVNQGDRESSIHLHGSPSRAPFDGWAEDLIMKGQFKDYYY	180
Db	121	DGISPGPTIIVPRGTEAVVRFINQGDRESSIHLHGSPSRAPFDGWADDMIMKGEYKDYYY	180
Qy	181	PNNQAARFLWYHDHAMHVTAENAYFGQAGAYLITDPAEDALGLPSGYGKYDIPLVLSSKF	240
Db	181	PNNQAARFLWYHDHAMHVTAENAYFGQAGAYLITDPAEDALGLPSGYGKYDIPLVLSSKY	240
Qy	241	YNSDGTLQTSVGEDNSLWGDVIHVNGQPWPFFNVEPRKYRLRFLNAAVSRNFALYFVKQQ	300
Db	241	YNADGTLKTSVGEDKSVWGDIIHVNGQPWPFLNVEPRKYRLRFLNAAVSRNFALYFVKQD	300
Qy	301	ATATRLPFQVIASDAGLLTHPVQTSDIYVAAAERYEIVFDFAPYAGQTIDLRNFAKANGV	360
Db	301	NTATRLPFQVIASDAGLLTHPVQTSDMYVAAAERYEIVFDFAPYAGQTLDLRNFAKANGI	360
Qy	361	GTDDDYANTDKVMRFHVSSQAVVDNSVVPAQLSQIQFPADKTGIDHHFRFHRTNSEWRIN	420
Db	361	GTDDDYANTDKVMRFHVSSQTVVDNSVVPEQLSQIQFPADKTDIDHHFRFHRTNGEWRIN	420
Qy	421	GIGFADVQNRILAKVPRGTVELWELENSSGGWSHPIHVHLVDFRVVARYGDESTRGVMPY	480
Db	421	GIGFADVENRVLAKVPRGTVELWELENSSGGWSHPIHVHLVDFRVVARYGDEGTRGVMPY	480
Qy	481	ESAGLKDVVWLGRHETVLVEAHYAPWDGVYMFHCHNLIHEDQDMMAAFDVTKLQNFGYNE :	540
Db	481	:	540
Qу	541	TTDFHDPEDSRWSARPFTAADLTARSGIFSEASIRARVNELALEQPYSELAQVTASLEQY	600
Db	541		600
Qу	601	YKTNKKRQAECEDMPAGPIPRYRRFQV 627	
Db	601	:	

•

```
Published_Applications_AA:*
Database :
                1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
                    /cgn2 6/ptodata/2/pubpaa/PCT NEW PUB.pep:*
                    /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
                    /cgn2 6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
                    /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
                5:
                    /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
                6:
                    /cqn2 6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
                7:
                    /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
                8:
                    /cgn2 6/ptodata/2/pubpaa/US09A PUBCOMB.pep:*
                9:
                10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
                11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
                12: /cgn2 6/ptodata/2/pubpaa/US09_NEW PUB.pep:*
                13: /cgn2 6/ptodata/2/pubpaa/US10A PUBCOMB.pep:*
                14: /cgn2 6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
                    /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
                    /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
                16:
                    /cgn2 6/ptodata/2/pubpaa/US60 NEW PUB.pep:*
                17:
                18: /cgn2 6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sult Query No. Score Match Length DB ID	Description
1 3336 100.0 627 13 US-10-080-210-7 2 3168 95.0 627 9 US-09-338-723A-4 3 3168 95.0 627 13 US-10-080-210-4 4 1929.5 57.8 594 9 US-09-338-723A-2 5 1929.5 57.8 594 13 US-10-080-210-2 6 1929.5 57.8 594 13 US-10-080-233-2 7 1795 53.8 572 9 US-09-942-185-4 8 1795 53.8 572 14 US-10-241-602-4	Sequence 7, Appli Sequence 4, Appli Sequence 4, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 4, Appli Sequence 4, Appli

Database :

PIR_78:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

					DOTTEMEND	
Result		% Query				
No.	Score	-	Length	DB	ID	Description
1	1795	53.8	572	2	B48521	bilirubin oxidase
2	689	20.7	513	2	F69604	spore coat protein
3	457.5	13.7	568	2	B86364	hypothetical prote
4	432.5	13.0	591	2	G96734	spore coat protein
5	427.5	12.8	527	2	C70397	periplasmic cell d
6	426.5	12.8	533	2	AC0414	probable exported
7	423	12.7	494	2	AC3582	probable blue-copp
8	412	12.4	516	2	C64735	probable copper-bi
9	409	12.3	516	2	G90644	hypothetical prote
10	409	12.3	516	2	G85495	hypothetical prote
11	390	11.7	536	2	AF0523	probable multicopp
12	320.5	9.6	470	2	E91116	suppressor of ftsI
13	320.5	9.6	470	2	E85961	suppressor of ftsI
14	319.5	9.6	470	2	G65088	sufI protein precu
15	310.5	9.3	470	2	AD0888	SufI protein [impo
16	296.5	8.9	513	2	G81298	probable periplasm
17	291	8.7	474	2	AD0083	probable cell divi
18	267	8.0	463	2	G83175	probable metallo-o
19	263	7.9	1662	2	T18540	mofA protein precu
20	250	7.5	721	2	H82528	L-ascorbate oxidas
21	233.5	7.0	311	2	H64157	sufI protein homol
22	225.5	6.8	500	2	B83910	hypothetical prote
23	217	6.5	520	2	JC5356	laccase (EC 1.10.3

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result Query No. Score Match Length DB ID Description 1 1795 53.8 572 1 BLRO_MYRVE Q12737 myrothect 2 689 20.7 513 1 COTA_BACSU P07788 bacillus 3 528.5 15.8 642 1 PHSA_STRAT Q53692 streptomy 4 426.5 12.8 533 1 CUEO_YERPE Q8zbk0 yersinia 5 412 12.4 516 1 CUEO_ECOLI P36649 escherich 6 409 12.3 516 1 CUEO_ECO57 Q8x947 escherich 7 390 11.7 536 1 CUEO SALTI Q8z9e1 salmonel	
2 689 20.7 513 1 COTA_BACSU P07788 bacillus 3 528.5 15.8 642 1 PHSA_STRAT Q53692 streptomy 4 426.5 12.8 533 1 CUEO_YERPE Q8zbk0 yersinia 5 412 12.4 516 1 CUEO_ECOLI P36649 escherich 6 409 12.3 516 1 CUEO_ECO57 Q8x947 escherich	
3 528.5 15.8 642 1 PHSA_STRAT Q53692 streptomy 4 426.5 12.8 533 1 CUEO_YERPE Q8zbk0 yersinia 5 412 12.4 516 1 CUEO_ECOLI P36649 escherich 6 409 12.3 516 1 CUEO_ECO57 Q8x947 escherich	
4 426.5 12.8 533 1 CUEO_YERPE Q8zbk0 yersinia 5 412 12.4 516 1 CUEO_ECOLI P36649 escherich 6 409 12.3 516 1 CUEO_ECO57 Q8x947 escherich	
5 412 12.4 516 1 CUEO_ECOLI P36649 escherich 6 409 12.3 516 1 CUEO_ECO57 Q8x947 escherich	
6 409 12.3 516 1 CUEO_ECO57 Q8x947 escherich	
7 200 11 7 E26 1 CUEO CALTI ORZGEI Salmoneli	
,	
8 390 11.7 536 1 CUEO_SALTY Q8zrs2 salmonell	
9 319.5 9.6 470 1 SUFI_ECOLI P26648 escherich	nia
10 310.5 9.3 470 1 SUFI_SALTY P40799 salmonel1	
11 233.5 7.0 311 1 SUFI_HAEIN P44847 haemophil	
12 217 6.5 520 1 LAC4_TRAVI Q99055 trametes	vi
13 216 6.5 520 1 LAC4_TRAVE Q12719 trametes	
14 210.5 6.3 591 1 LAC1_CRYPA Q03966 cryphoneo	ctr
15 210 6.3 619 1 LAC1_NEUCR P06811 neurospor	ra
16 200 6.0 619 1 LAC2_NEUCR P10574 neurospor	
17 197 5.9 529 1 LAC1_PLEOS Q12729 pleurotus	
18 195.5 5.9 533 1 LAC2_PLEOS Q12739 pleurotus	
19 194 5.8 589 1 CPA2_PSESM P59571 pseudomor	nas

Database : SPTREMBL_25:* 1: sp_archea:* 2: sp_bacteria:* 3: sp_fungi:* 4: sp_human:* 5: sp_invertebrate:* 6: sp_mammal:* 7: sp_mhc:* 8: sp_organelle:* 9: sp_phage:* 10: sp_plant:* 11: sp_rodent:* 12: sp_virus:* 13: sp_vertebrate:* 14: sp_unclassified:* 15: sp_rvirus:*
16: sp_bacteriap:* 17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	용				
	Query				
Score	Match	Length	DB	ID	Description
1761 5	52.8	602	· 3	 .09P8C3	Opp8c3 acremonium
624.5	18.7	475	2	Q93M03	Q93m03 streptomyce
611	18.3	513	16	Q8CXJ7	Q8cxj7 oceanobacil
534	16.0	431	2	Q8RMC6	Q8rmc6 streptomyce
513.5	15.4	631	2	Q8GB87	Q8gb87 streptomyce
508	15.2	583	16	Q8FQU9	Q8fqu9 corynebacte
487	14.6	511	16	Q8NRU6	Q8nru6 corynebacte
483.5	14.5	582	10	Q9AWU4	Q9awu4 oryza sativ
467.5	14.0	637	10	Q9FTS3	Q9fts3 oryza sativ
467	14.0	501	16	Q88ZG5	Q88zg5 lactobacill
	1761.5 624.5 611 534 513.5 508 487 483.5 467.5	Score Match 1761.5 52.8 624.5 18.7 611 18.3 534 16.0 513.5 15.4 508 15.2 487 14.6 483.5 14.5 467.5 14.0	Query Score Match Length 1761.5 52.8 602 624.5 18.7 475 611 18.3 513 534 16.0 431 513.5 15.4 631 508 15.2 583 487 14.6 511 483.5 14.5 582 467.5 14.0 637	Query Score Match Length DB 1761.5 52.8 602 3 624.5 18.7 475 2 611 18.3 513 16 534 16.0 431 2 513.5 15.4 631 2 508 15.2 583 16 487 14.6 511 16 483.5 14.5 582 10 467.5 14.0 637 10	Query Score Match Length DB ID 1761.5 52.8 602 3 Q9P8C3 624.5 18.7 475 2 Q93M03 611 18.3 513 16 Q8CXJ7 534 16.0 431 2 Q8RMC6 513.5 15.4 631 2 Q8GB87 508 15.2 583 16 Q8FQU9 487 14.6 511 16 Q8NRU6 483.5 14.5 582 10 Q9AWU4 467.5 14.0 637 10 Q9FTS3

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RESULT 2
AR275740
                                            linear PAT 10-APR-2003
                             858 bp
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LOCUS
         AR275740
         Sequence 8 from patent US 6509307.
DEFINITION
         AR275740
ACCESSION
         AR275740.1 GI:29709289
VERSION
KEYWORDS
SOURCE
         Unknown.
 ORGANISM
         Unknown.
         Unclassified.
            (bases 1 to 858)
REFERENCE
         Bodie, E.A., van der Velden, S., de Vries, C.H. and Wang, H.
 AUTHORS
         Detergent compositions comprising phenol oxidizing enzymes from
 TITLE
         Patent: US 6509307-A 8 21-JAN-2003;
 JOURNAL
FEATURES
                Location/Qualifiers
                1. .858
    source
                 /organism="unknown"
                 /mol type="genomic DNA"
ORIGIN
                     99.0%; Score 849; DB 6; Length 858;
 Query Match
 Best Local Similarity 100.0%; Pred. No. 5.6e-206;
                                                       Gaps
                                                              0;
 Matches 858; Conservative
                          0; Mismatches
                                         0: Indels
                                                    0;
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Qу
           1 CACCGCCGAGAACGCTTACTTTGGTCAAGCTGGCTTTTACATTCTGCACGACCCCGCTGA 60
Db
         61 AGATGCATTGGGTCTGCCTTCTGGCAAGTATGATGTACCTCTTGCACTGTCCTCCAAGCA 120
Qу
           61 AGATGCATTGGGTCTGCCTTCTGGCAAGTATGATGTACCTCTTGCACTGTCCTCCAAGCA 120
Db
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Qу
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Db
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           181 TGTCATCCACGTCAACGGACAGCCATGGCCCTACTTTAAGGTCGAGCCTCGCAAGTACCG 240
Db
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Qу
           241 TCTCCGCTTCCTCAATGCTGCTATCAGCCGTGCCTTCAAGCTCACTTTCGAGGCTGATGG 300
Db
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Qу
           301 CAAAGTGATCAACTTTCCTGTCATCGGTGCCGATACTGGTCTCTTGACCAAGCCTGTTCA 360
Db
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Ov
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Db
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Qу
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Db
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Qy	481	CAACTCCACCGACAAAGTCATGCAGTTCGTTGTTGGCAAGGATGTTACGAGCCAGGCTGG	540
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Qy	541	TAATGGCAACCTTCCCGGCTCTCTGCGCACTGTTCCCTTCCCTCCTAAGAAGGGGCGGAG	600
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Qy	601	TCGACAGGAGCTTCAAGTTCGGCAGGGACCGGTGGCCAGTGGACTGTTAATGGCTTGACC	660
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Qу	661	TTCGCTGATGTCAACAACCGCATCCTGGCTAAGCCCCCAACGTGGTGCCATCGAGGTTTT	720
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Qy	721	GGGAGCTTTGAGAACTTCCAGCGGNGGNTGGTCTTACCCTTGTCCACATCCACCTGGGTC	780
Db	721	GGGAGCTTTGAGAACTTCCAGCGGNGGNTGGTCTTACCCTTGTCCACATCCACCTGGGTC	780
Qy	781	GACTTTCCAGATNCTTGTCTTGCACTGGANGCAAGGCNCCCCGTTNTAACTNCNANAAAG	840
Db	781	GACTTTCCAGATNCTTGTCTTGCACTGGANGCAAGGCNCCCCGTTNTAACTNCNANAAAG	840
Qy	841	GAAGCACTTTCAAGGGCG 858	
Db	841	GAAGCACTTTCAAGGGCG 858	

Result		% Query				
No.	Score	Match	Length	DB	ID	Description
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2	3168	95.0	627	17	US-09-338-723-4	Sequence 4, Appli
3	3168	95.0	627	17	US-09-338-723A-4	Sequence 4, Appli
4	3168	95.0	627	26	US-10-080-210-4	Sequence 4, Appli
5	1929.5	57.8	594	16	US-09-218-702-2	Sequence 2, Appli
6	1929.5	57.8	594	16	US-09-273-957-2	Sequence 2, Appli
7	1929.5	57.8	594	17	US-09-338-723-2	Sequence 2, Appli
8	1929.5	57.8	594	17	US-09-338-723A-2	Sequence 2, Appli